



SEQUENCE LISTING

<110> YIP, CEC

<120> IDENTIFICATION OF COMPOUNDS FOR MODULATING DIMERIC RECEPTORS

<130> P04885US1

<140> 09/744628

<141> 2000-05-25

<150> PCT/CA00/00605

<151> 2000-05-25

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> X(1)=N,Q,T,Y X(2)=K,R X(3)=A,L,I,P,F,W,M,C,G
X(4)=D X(5)=Q,S,T,N X(6)=A,V,I,P,F,W,M,C,G
X(7)=D X(8)=K,H X(9)=A,V,I,P,L,W,M,C,G
X(10)=A,V,I,P,L,W,M,C,G X(11)=Q,S,T,N X(12)=H,R

<400> 1

Phe Val Asn Gln His Leu Cys Gly Xaa Xaa Leu Xaa Xaa Ala Leu Xaa
1 5 10 15

Xaa Val Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Thr Pro Xaa Thr
20 25 30

<210> 2

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> X(1)=D X(2)=Q,S,T,Y
X(3)=N,Q,S,T,Y X(4)=,Q,S,T,Y
X(5)=D X(6)=Q,S,T,Y

<400> 2

Gly Ile Val Xaa Xaa Cys Cys Xaa Ser Ile Cys Ser Leu Tyr Xaa Leu
1 5 10 15

Xaa Asn Tyr Cys Xaa
20

<210> 3

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> X(1)=N,Q,T,Y X(2)=K,R X(3)=A,L,I,P,F,W,M,C,G X(4)=D

X(5)=Q,S,T,N X(6)=A,V,I,P,F,W,M,C,G X(7)=D X(8)=K,H
 X(9)=A,V,I,P,L,W,M,C,G X(10)=A,V,I,P,L,W,M,C,G X(11)=Q,S,T,N
 X(13)=H,R

<400> 3

Phe	Val	Asn	Gln	His	Leu	Cys	Gly	Xaa	Xaa	Leu	Xaa	Xaa	Ala	Leu	Xaa
1				5				10						15	
Xaa	Val	Cys	Gly	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Thr	Xaa	Pro	Thr		
			20				25						30		

<210> 4

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> X(1)=D X(2)=Q,S,T,Y
 X(3)=N,Q,S,T,Y X(4)=Q,S,T,Y
 X(5)=D X(6)=Q,S,T,Y

<400> 4

Gly	Ile	Val	Xaa	Xaa	Cys	Cys	Xaa	Ser	Ile	Cys	Ser	Leu	Tyr	Xaa	Leu
1				5				10						15	
Xaa	Asn	Tyr	Cys	Xaa											
			20												

<210> 5

<211> 30

<212> PRT

<213> Bos taurus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> X(1)=N,Q,T,Y X(2)=K,R X(3)=A,L,I,P,F,W,M,C,G
X(4)=D X(5)=Q,S,T,N X(6)=A,V,I,P,F,W,M,C,G
X(7)=D X(8)=K,H X(9)=A,V,I,P,L,W,M,C,G
X(10)=A,V,I,P,L,W,M,C,G X(11)=Q,S,T,N X(12)=H,R

<400> 5

Phe Val Asn Gln His Leu Cys Gly Xaa Xaa Leu Xaa Xaa Ala Leu Xaa
1 5 10 15

Xaa Val Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Thr Pro Xaa Ala
20 25 30

<210> 6

<211> 21

<212> PRT

<213> Bos taurus

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> X(1)=D X(2)=Q,S,T,Y
X(3)=N,Q,S,T,Y X(4)=Q,S,T,Y
X(5)=D X(6)=Q,S,T,Y

<400> 6

Gly Ile Val Xaa Xaa Cys Cys Xaa Ser Val Cys Ser Leu Tyr Xaa Leu
1 5 10 15

Xaa Asn Tyr Cys Xaa
20

<210> 7

<211> 30

<212> PRT

<213> Sus scrofa

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> X(1)=N,Q,T,Y X(2)=K,R X(3)=A,L,I,P,F,W,M,C,G
X(4)=D X(5)=Q,S,T,N X(6)=A,V,I,P,F,W,M,C,G
X(7)=D X(8)=K,H X(9)=A,V,I,P,L,W,M,C,G
X(10)=A,V,I,P,L,W,M,C,G X(11)=Q,S,T,N X(12)=H,R

<400> 7

Phe Val Asn Gln His Leu Cys Gly Xaa Xaa Leu Xaa Xaa Ala Leu Xaa
1 5 10 15

Xaa Val Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Thr Pro Xaa Ala
20 25 30

<210> 8

<211> 21

<212> PRT

<213> Sus scrofa

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> X(1)=D X(2)=Q,S,T,Y
X(3)=N,Q,S,T,Y X(4)=Q,S,T,Y
X(5)=D X(6)=Q,S,T,Y

<400> 8

Gly Ile Val Xaa Xaa Cys Cys Xaa Ser Ile Cys Ser Leu Tyr Xaa Leu
1 5 10 15

Xaa Asn Tyr Cys Xaa
20

<210> 9

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(30)

<400> 9

Phe	Val	Asn	Gln	His	Leu	Cys	Gly	Ser	His	Leu	Val	Glu	Ala	Leu	Tyr
1				5				10						15	
Leu	Val	Cys	Gly	Glu	Arg	Gly	Phe	Phe	Tyr	Thr	Pro	Lys	Thr		
			20					25					30		

<210> 10

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(21)

<400> 10

Gly	Ile	Val	Glu	Gln	Cys	Cys	Thr	Ser	Ile	Cys	Ser	Leu	Tyr	Gln	Leu
1				5				10						15	
Glu	Asn	Tyr	Cys	Asn											
			20												

<210> 11

<211> 30

<212> PRT

<213> Bos taurus

<220>

<221> PEPTIDE

<222> (1)..(30)

<400> 11

Phe	Val	Asn	Gln	His	Leu	Cys	Gly	Ser	His	Leu	Val	Glu	Ala	Leu	Tyr
1				5				10						15	

Leu	Val	Cys	Gly	Glu	Arg	Gly	Phe	Phe	Tyr	Thr	Pro	Lys	Ala
			20				25						30

<210> 12

<211> 21

<212> PRT

<213> Bos taurus

<220>

<221> PEPTIDE

<222> (1)..(21)

<400> 12

Gly	Ile	Val	Glu	Gln	Cys	Cys	Ala	Ser	Val	Cys	Ser	Leu	Tyr	Gln	Leu
1				5				10						15	

Glu	Asn	Tyr	Cys	Asn
			20	

<210> 13

<211> 30

<212> PRT

<213> Sus scrofa

<220>

<221> PEPTIDE

<222> (1)..(30)

<400> 13

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Ala
20 25 30

<210> 14

<211> 21

<212> PRT

<213> Sus scrofa

<220>

<221> PEPTIDE

<222> (1)..(21)

<400> 14

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
1 5 10 15

Glu Asn Tyr Cys Asn
20

<210> 15

<211> 27

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(27)

<400> 15

Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val
 1 5 10 15

Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly
 20 25

<210> 16

<211> 719

<212> PRT

<213> Homo sapiens

<220>

<221> CHAIN

<222> (1)..(719)

<400> 16

His Leu Tyr Pro Gly Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn
 1 5 10 15

Leu Thr Arg Leu His Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His
 20 25 30

Leu Gln Ile Leu Leu Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp
 35 40 45

Leu Ser Phe Pro Lys Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe
 50 55 60

Arg Val Tyr Gly Leu Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr
 65 70 75 80

Val Ile Arg Gly Ser Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe
 85 90 95

Glu Met Val His Leu Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile
 100 105 110

Thr Arg Gly Ser Val Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu
 115 120 125

Ala Thr Ile Asp Trp Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His
 130 135 140

Ile Val Leu Asn Lys Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro
 145 150 155 160

Gly Thr Ala Lys Gly Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly

165								170				175			
Gln	Phe	Val	Glu	Arg	Cys	Trp	Thr	His	Ser	His	Cys	Gln	Lys	Val	Cys
			180								185				190
Pro	Thr	Ile	Cys	Lys	Ser	His	Gly	Cys	Thr	Ala	Glu	Gly	Leu	Cys	Cys
			195				200						205		
His	Ser	Glu	Cys	Leu	Gly	Asn	Cys	Ser	Gln	Pro	Asp	Asp	Pro	Thr	Lys
			210				215					220			
Cys	Val	Ala	Cys	Arg	Asn	Phe	Tyr	Leu	Asp	Gly	Arg	Cys	Val	Glu	Thr
						230					235				240
Cys	Pro	Pro	Pro	Tyr	Tyr	His	Phe	Gln	Asp	Trp	Arg	Cys	Val	Asn	Phe
						245					250				255
Ser	Phe	Cys	Gln	Asp	Leu	His	His	Lys	Cys	Lys	Asn	Ser	Arg	Arg	Gln
						260								270	
Gly	Cys	His	Gln	Tyr	Val	Ile	His	Asn	Asn	Lys	Cys	Ile	Pro	Glu	Cys
			275				280						285		
Pro	Ser	Gly	Tyr	Thr	Met	Asn	Ser	Ser	Asn	Leu	Leu	Cys	Thr	Pro	Cys
						295						300			
Leu	Gly	Pro	Cys	Pro	Lys	Val	Cys	His	Leu	Leu	Glu	Gly	Glu	Lys	Thr
						310					315				320
Ile	Asp	Ser	Val	Thr	Ser	Ala	Gln	Glu	Leu	Arg	Gly	Cys	Thr	Val	Ile
						325									335
Asn	Gly	Ser	Leu	Ile	Ile	Asn	Ile	Arg	Gly	Gly	Asn	Asn	Leu	Ala	Ala
						340								350	
Glu	Leu	Glu	Ala	Asn	Leu	Gly	Leu	Ile	Glu	Glu	Ile	Ser	Gly	Tyr	Leu
						355							365		
Lys	Ile	Arg	Arg	Ser	Tyr	Ala	Leu	Val	Ser	Leu	Ser	Phe	Phe	Arg	Lys
						375						380			
Leu	Arg	Leu	Ile	Arg	Gly	Glu	Thr	Leu	Glu	Ile	Gly	Asn	Tyr	Ser	Phe
						390					395				400
Tyr	Ala	Leu	Asp	Asn	Gln	Asn	Leu	Arg	Gln	Leu	Trp	Asp	Trp	Ser	Lys
						405						410			415
His	Asn	Leu	Thr	Thr	Thr	Gln	Gly	Lys	Leu	Phe	Phe	His	Tyr	Asn	Pro
						420								430	
Lys	Leu	Cys	Leu	Ser	Glu	Ile	His	Lys	Met	Glu	Glu	Val	Ser	Gly	Thr
						435								445	
Lys	Gly	Arg	Gln	Glu	Arg	Asn	Asp	Ile	Ala	Leu	Lys	Thr	Asn	Gly	Asp
						450						460			
Lys	Ala	Ser	Cys	Glu	Asn	Glu	Leu	Leu	Lys	Phe	Ser	Tyr	Ile	Arg	Thr

465		470		475		480
Ser Phe Asp Lys Ile Leu Leu Arg Trp Glu Pro Tyr Trp Pro Pro Asp						
	485			490		495
Phe Arg Asp Leu Leu Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr						
	500		505		510	
Gln Asn Val Thr Glu Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser						
	515		520		525	
Trp Thr Val Val Asp Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys						
	530		535		540	
Ser Gln Asn His Pro Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr						
545		550		555		560
Gln Tyr Ala Ile Phe Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg						
	565		570			575
Arg Thr Tyr Gly Ala Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala						
	580		585			590
Thr Asn Pro Ser Val Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser						
	595		600		605	
Ser Gln Ile Ile Leu Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn						
610		615		620		
Ile Thr His Tyr Leu Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu						
625		630		635		640
Leu Phe Glu Leu Asp Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg						
	645		650			655
Thr Trp Ser Pro Pro Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln						
	660		665			670
Ser Glu Tyr Glu Asp Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr						
	675		680		685	
Asp Ser Gln Ile Leu Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr						
690		695		700		
Phe Glu Asp Tyr Leu His Asn Val Val Phe Val Pro Arg Pro Ser						
705		710		715		

<210> 17

<211> 620

<212> PRT

<213> Homo sapiens

<220>

<221> CHAIN

<222> (1)..(620)

<400> 17

Ser Leu Gly Asp Val Gly Asn Val Thr Val Ala Val Pro Thr Val Ala
1 5 10 15

Ala Phe Pro Asn Thr Ser Ser Thr Ser Val Pro Thr Ser Pro Glu Glu
20 25 30

His Arg Pro Phe Glu Lys Val Val Asn Lys Glu Ser Leu Val Ile Ser
35 40 45

Gly Leu Arg His Phe Thr Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn
50 55 60

Gln Asp Thr Pro Glu Glu Arg Cys Ser Val Ala Ala Tyr Val Ser Ala
65 70 75 80

Arg Thr Met Pro Glu Ala Lys Ala Asp Asp Ile Val Gly Pro Val Thr
85 90 95

His Glu Ile Phe Glu Asn Asn Val Val His Leu Met Trp Gln Glu Pro
100 105 110

Lys Glu Pro Asn Gly Leu Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg
115 120 125

Tyr Gly Asp Glu Glu Leu His Leu Cys Val Ser Arg Lys His Phe Ala
130 135 140

Leu Glu Arg Gly Cys Arg Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser
145 150 155 160

Val Arg Ile Arg Ala Thr Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu
165 170 175

Pro Thr Tyr Phe Tyr Val Thr Asp Tyr Leu Asp Val Pro Ser Asn Ile
180 185 190

Ala Lys Ile Ile Ile Gly Pro Leu Ile Phe Val Phe Leu Phe Ser Val
195 200 205

Val Ile Gly Ser Ile Tyr Leu Phe Leu Arg Lys Arg Gln Pro Asp Gly
210 215 220

Pro Leu Gly Pro Leu Tyr Ala Ser Ser Asn Pro Glu Tyr Leu Ser Ala
225 230 235 240

Ser Asp Val Phe Pro Cys Ser Val Tyr Val Pro Asp Glu Trp Glu Val
245 250 255

Ser	Arg	Glu	Lys	Ile	Thr	Leu	Leu	Arg	Glu	Leu	Gly	Gln	Gly	Ser	Phe	260	265	270
Gly	Met	Val	Tyr	Glu	Gly	Asn	Ala	Arg	Asp	Ile	Ile	Lys	Gly	Glu	Ala	275	280	285
Glu	Thr	Arg	Val	Ala	Val	Lys	Thr	Val	Asn	Glu	Ser	Ala	Ser	Leu	Arg	290	295	300
Glu	Arg	Ile	Glu	Phe	Leu	Asn	Glu	Ala	Ser	Val	Met	Lys	Gly	Phe	Thr	305	310	315
Cys	His	His	Val	Val	Arg	Leu	Leu	Gly	Val	Val	Ser	Lys	Gly	Gln	Pro	325	330	335
Thr	Leu	Val	Val	Met	Glu	Leu	Met	Ala	His	Gly	Asp	Leu	Lys	Ser	Tyr	340	345	350
Leu	Arg	Ser	Leu	Arg	Pro	Glu	Ala	Glu	Asn	Asn	Pro	Gly	Arg	Pro	Pro	355	360	365
Pro	Thr	Leu	Gln	Glu	Met	Ile	Gln	Met	Ala	Ala	Glu	Ile	Ala	Asp	Gly	370	375	380
Met	Ala	Tyr	Leu	Asn	Ala	Lys	Lys	Phe	Val	His	Arg	Asp	Leu	Ala	Ala	385	390	395
Arg	Asn	Cys	Met	Val	Ala	His	Asp	Phe	Thr	Val	Lys	Ile	Gly	Asp	Phe	405	410	415
Gly	Met	Thr	Arg	Asp	Ile	Tyr	Glu	Thr	Asp	Tyr	Tyr	Arg	Lys	Gly	Gly	420	425	430
Lys	Gly	Leu	Leu	Pro	Val	Arg	Trp	Met	Ala	Pro	Glu	Ser	Leu	Lys	Asp	435	440	445
Gly	Val	Phe	Thr	Thr	Ser	Ser	Asp	Met	Trp	Ser	Phe	Gly	Val	Val	Leu	450	455	460
Trp	Glu	Ile	Thr	Ser	Leu	Ala	Glu	Gln	Pro	Tyr	Gln	Gly	Leu	Ser	Asn	465	470	475
Glu	Gln	Val	Leu	Lys	Phe	Val	Met	Asp	Gly	Gly	Tyr	Leu	Asp	Gln	Pro	485	490	495
Asp	Asn	Cys	Pro	Glu	Arg	Val	Thr	Asp	Leu	Met	Arg	Met	Cys	Trp	Gln	500	505	510
Phe	Asn	Pro	Lys	Met	Arg	Pro	Thr	Phe	Leu	Glu	Ile	Val	Asn	Leu	Leu	515	520	525
Lys	Asp	Asp	Leu	His	Pro	Ser	Phe	Pro	Glu	Val	Ser	Phe	Phe	His	Ser	530	535	540
Glu	Glu	Asn	Lys	Ala	Pro	Glu	Ser	Glu	Glu	Leu	Glu	Met	Glu	Phe	Glu	545	550	555
																		560

Asp	Met	Glu	Asn	Val	Pro	Leu	Asp	Arg	Ser	Ser	His	Cys	Gln	Arg	Glu
			565						570					575	
Glu	Ala	Gly	Gly	Arg	Asp	Gly	Gly	Ser	Ser	Leu	Gly	Phe	Lys	Arg	Ser
		580						585					590		
Tyr	Glu	Glu	His	Ile	Pro	Tyr	Thr	His	Met	Asn	Gly	Gly	Lys	Lys	Asn
	595						600					605			
Gly	Arg	Ile	Leu	Thr	Leu	Pro	Arg	Ser	Asn	Pro	Ser				
	610					615					620				